



33769-701.831.txt
SEQUENCE LISTING

<110> Hengst, Ludger
Cilensek, Zoran
Grimmler, Matthias

<120> Tyrosine phosphorylation of CDK Inhibitor Proteins of the Cip/Kip Family

<130> 33769-701.831

<140> US 10/576,845

<141> 2004-10-20

<160> 25

<170> PatentIn version 3.2

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<212> DNA

<213> Homo sapiens

<400> 1

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ttaacccggg acttgagaa gactgcaga gacatggaag aggcgagcca gcgcaagtgg      180
aatttcgatt ttcagaatca caaaccccta gagggcaagt acgagtggca agagggtggag      240
aagggcagct tgcccagatt ctactacaga ccccgcggc ccccaaaagg tgcctgcaag      300
gtgccggcgc aggagagcca ggatgtcagc gggagccgcc cggcggcgcc ttttaattggg      360
gctccggcta actctgagga cacgcatttg gtggacccaa agactgatcc gtcggacagc      420
cagacggggt tagcggagca atgcgcagga ataaggaagc gacctgcaac cgacgattct      480
tctactcaaa acaaaagagc caacagaaca gaagaaaatg tttcagacgg ttccccaat      540
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Asp Ala Arg Gln Ala Glu His Pro Lys Pro Ser Ala Cys Arg Asn Leu
20           25           30
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Phe Gly Pro Val Asp His Glu Glu Leu Thr Arg Asp Leu Glu Lys His
35           40           45
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Cys Arg Asp Met Glu Glu Ala Ser Gln Arg Lys Trp Asn Phe Asp Phe
50 55 60

Gln Asn His Lys Pro Leu Glu Gly Lys Tyr Glu Trp Gln Glu Val Glu
65 70 75 80

Lys Gly Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro Pro Lys
85 90 95

Gly Ala Cys Lys Val Pro Ala Gln Glu Ser Gln Asp Val Ser Gly Ser
100 105 110

Arg Pro Ala Ala Pro Leu Ile Gly Ala Pro Ala Asn Ser Glu Asp Thr
115 120 125

His Leu Val Asp Pro Lys Thr Asp Pro Ser Asp Ser Gln Thr Gly Leu
130 135 140

Ala Glu Gln Cys Ala Gly Ile Arg Lys Arg Pro Ala Thr Asp Asp Ser
145 150 155 160

Ser Thr Gln Asn Lys Arg Ala Asn Arg Thr Glu Glu Asn Val Ser Asp
165 170 175

Gly Ser Pro Asn Ala Gly Ser Val Glu Gln Thr Pro Lys Lys Pro Gly
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Leu Arg Arg Arg Gln Thr
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tgcattcagg agggccgtga gcgatggaac ttcgactttg tcaccgagac accactggag 180
ggtgacttcg cctgggagcg tgtgcggggc cttggcctgc ccaagctcta ccttcccacg 240
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ctgctgcagg ggacagcaga ggaagaccat gtggacctgt cactgtcttg tacccttggtg 360
cctcgctcag gggagcaggc tgaagggtcc ccaggtggac ctggagactc tcagggtcga 420
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aagaggaagc cctaa 495

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 20 25 30

Asp Cys Asp Ala Leu Met Ala Gly Cys Ile Gln Glu Ala Arg Glu Arg
 35 40 45

Trp Asn Phe Asp Phe Val Thr Glu Thr Pro Leu Glu Gly Asp Phe Ala
 50 55 60

Trp Glu Arg Val Arg Gly Leu Gly Leu Pro Lys Leu Tyr Leu Pro Thr
 65 70 75 80

Gly Pro Arg Arg Gly Arg Asp Glu Leu Gly Gly Gly Arg Arg Pro Gly
 85 90 95

Thr Ser Pro Ala Leu Leu Gln Gly Thr Ala Glu Glu Asp His Val Asp
 100 105 110

Leu Ser Leu Ser Cys Thr Leu Val Pro Arg Ser Gly Glu Gln Ala Glu
 115 120 125

Gly Ser Pro Gly Gly Pro Gly Asp Ser Gln Gly Arg Lys Arg Arg Gln
 130 135 140

Thr Ser Met Thr Asp Phe Tyr His Ser Lys Arg Arg Leu Ile Phe Ser
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Lys Arg Lys Pro

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Leu Phe Gly Pro Val Asp His Glu Glu Leu Ser Arg Glu Leu Gln Ala
35 40 45

Arg Leu Ala Glu Leu Asn Ala Glu Asp Gln Asn Arg Trp Asp Tyr Asp
50 55 60

Phe Gln Gln Asp Met Pro Leu Arg Gly Pro Gly Arg Leu Gln Trp Thr
65 70 75 80

Glu Val Asp Ser Asp Ser Val Pro Ala Phe Tyr Arg Glu Thr Val Gln
85 90 95

Val Gly Arg Cys Arg Leu Leu Leu Ala Pro Arg Pro Val Ala Val Ala
100 105 110

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Val Ala Val Ser Pro Pro Leu Glu Pro Ala Ala Glu Ser Leu Asp Gly
115 120 125

Leu Glu Glu Ala Pro Glu Gln Leu Pro Ser Val Pro Val Pro Ala Pro
130 135 140

Ala Ser Thr Pro Pro Pro Val Pro Val Leu Ala Pro Ala Pro Ala Pro
145 150 155 160

Ala Pro Ala Pro Val Ala Ala Pro Val Ala Ala Pro Val Ala Val Ala
165 170 175

Val Leu Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro
180 185 190

Ala Pro Val Ala Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro
195 200 205

Ala Pro Ala Pro Ala Pro Ala Pro Asp Ala Ala Pro Gln Glu Ser Ala
210 215 220

Glu Gln Gly Ala Asn Gln Gly Gln Arg Gly Gln Glu Pro Leu Ala Asp
225 230 235 240

Gln Leu His Ser Gly Ile Ser Gly Arg Pro Ala Ala Gly Thr Ala Ala
245 250 255

Ala Ser Ala Asn Gly Ala Ala Ile Lys Lys Leu Ser Gly Pro Leu Ile
260 265 270

Ser Asp Phe Phe Ala Lys Arg Lys Arg Ser Ala Pro Glu Lys Ser Ser
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Gly Ser Val Glu Gln Thr Pro Arg Lys Arg Leu Arg
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<400> 17
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